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Fig. 1(ii)

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Fig.1(iv)

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CTG TCT TGG GTG CAT TGG AGC	49
Leu Ser Trp Val His Trp Ser	
5 10	
CAT GCC AAG TGG TCC CAG GCT GCA	97
His Ala Lys Trp Ser Gln Ala Ala	
20 25	
AAT CAT CAC GAA GTG GTG AAG TTC	145
Asn His His Glu Val Val Lys Phe	
40	
TGC CAT CCA ATC GAG ACC CTG GTG	193
Cys His Pro Ile Glu Thr Leu Val	
55	
GAG ATC GAG TAC ATC TTC AAG CCA	241
Glu Ile Glu Tyr Ile Phe Lys Pro	
70 75	
GGG GGC TGC TGC AAT GAC GAG GGC	289
Gly Gly Cys Cys Asn Asp Glu Gly	
85 90	
TCC AAC ATC ACC ATG CAG ATT ATG	337
Ser Asn Ile Thr Met Gln Ile Met	
100 105	
CAC ATA GGA GAG ATG AGC TTC CTA	385
His Ile Gly Glu Met Ser Phe Leu	
120	

Fig.1(iii)

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1	TCGGCCTCC GAAACC ATG AAC TTT CTG	
	Met Asn Phe Leu	
	1	
50	CTT GCC TTG CTG CTC TAC CTC CAC	
	Leu Ala Leu Leu Leu Tyr Leu His	
	15	
98	CCC ATG GCA GAA GGA GGA GGG CAG	
	Pro Met Ala Glu Gly Gly Gly Gln	
	30	35
146	ATG GAT GTC TAT CAG CGC AGC TAC	
	Met Asp Val Tyr Gln Arg Ser Tyr	
	45	50
194	GAC ATC TTC CAG GAG TAC CCT GAT	
	Asp Ile Phe Gln Glu Tyr Pro Asp	
	60	65
242	TCC TGT GTG CCC CTG ATG CGA TGC	
	Ser Cys Val Pro Leu Met Arg Cys	
	80	
290	CTC GAG TGT GTG CCC ACT GAG GAG	
	Leu Glu Cys Val Pro Thr Glu Glu	
	95	
338	CGG ATC AAA CCT CAC CAA GGC CAG	
	Arg Ily Lys Pro His Gln Gly Gln	
	110	115

Fig.1(i)

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386	CAG	CAC	AAC	AAA	TGT	GAA	TGC	AGA
	Gln	His	Asn	Lys	Cys	Glu	Cys	Arg
		125					130	
434	GAA	AAT	CCC	TGT	GGG	CCT	TGC	TCA
	Glu	Asn	Pro	Cys	Gly	Pro	Cys	Ser
	140					145		
482	CAA	GAT	CCG	CAG	ACG	TGT	AAA	TGT
	Gln	Asp	Pro	Gln	Thr	Cys	Lys	Cys
					160			
530	TGC	AAG	GCG	AGG	CAG	CTT	GAG	TTA
	Cys	Lys	Ala	Arg	Gln	Leu	Glu	Leu
				175				
578	AAG	CCG	AGG	CGG	TGAGCCGGGC	AGGAG		
	Lys	Pro	Arg	Arg				
			190					
630	GAACCAGATC	TCTCACCAGG						

Fig.1(iii)

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CCA	AAG	AAA	GAT	AGA	GCA	AGA	CAA	433
Pro	Lys	Lys	Asp	Arg	Ala	Arg	Gln	
			135					
GAG	CGG	AGA	AAG	CAT	TTG	TTT	GTA	481
Glu	Arg	Arg	Lys	His	Leu	Phe	Val	
		150					155	
TCC	TGC	AAA	AAC	ACA	GAC	TCG	CGT	529
Ser	Cys	Lys	Asn	Thr	Asp	Ser	Arg	
	165					170		
AAC	GAA	CGT	ACT	TGC	AGA	TGT	GAC	577
Asn	Glu	Arg	Thr	Cys	Arg	Cys	Asp	
180					185			
GAAGG	AGCCTCCCTC	AGCGTTTCGG						629
								649

Fig.1(iv)

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<p>7/52</p> <p><i>Fig. 2(i)</i></p>	<p>8/52</p> <p><i>Fig. 2(ii)</i></p>
<p>9/52</p> <p><i>Fig 2(iii)</i></p>	<p>10/52</p> <p><i>Fig 2(iv)</i></p>
<p>11/52</p> <p><i>Fig 2(v)</i></p>	<p>12/52</p> <p><i>Fig 2(vi)</i></p>

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1	CC ATG AGC CCT CTG CTC CGC CGC	
	Met Ser Pro Leu Leu Arg Arg	
	1 5	
48	CTG GCC CCC GCC CAG GCC CCT GTC	
	Leu Ala Pro Ala Gln Ala Pro Val	
	20	
96	CAG AGG AAA GTG GTG TCA TGG ATA	
	Gln Arg Lys Val Val Ser Trp Ile	
	35	
144	CAG CCC CGG GAG GTG GTG GTG CCC	
	Gln Pro Arg Glu Val Val Val Pro	
	50 55	
192	GTG GCC AAA CAG CTG GTG CCC AGC	
	Val Ala Lys Gln Leu Val Pro Ser	
	65 70	
240	GGC TGC TGC CCT GAC GAT GGC CTG	
	Gly Cys Cys Pro Asp Asp Gly Leu	
	80 85	
288	CAA GTC CGG ATG CAG ATC CTC ATG	
	Gln Val Arg Met Gln Ile Leu Met	
	100	
336	GGG GAG ATG TCC CTG GAA GAA CAC	
	Gly Glu Met Ser Leu Glu Glu His	
	115	

Fig.2(i)

8/52

CTG	CTG	CTC	GCC	GCA	CTC	CTG	CAG	47
Leu	Leu	Leu	Ala	Ala	Leu	Leu	Gln	
		10					15	
TCC	CAG	CCT	GAT	GCC	CCT	GGC	CAC	95
Ser	Gln	Pro	Asp	Ala	Pro	Gly	His	
	25					30		
GAT	GTG	TAT	ACT	CGC	GCT	ACC	TGC	143
Asp	Val	Tyr	Thr	Arg	Ala	Thr	Cys	
40					45			
TTG	ACT	GTG	GAG	CTC	ATG	GGC	ACC	191
Leu	Thr	Val	Glu	Leu	Met	Gly	Thr	
			60					
TGC	GTG	ACT	GTG	CAG	CGC	TGT	GGT	239
Cys	Val	Thr	Val	Gln	Arg	Cys	Gly	
			75					
GAG	TGT	GTG	CCC	ACT	GGG	CAG	CAC	287
Glu	Cys	Val	Pro	Thr	Gly	Gln	His	
		90					95	
ATC	CGG	TAC	CCG	AGC	AGT	CAG	CTG	335
Ile	Arg	Tyr	Pro	Ser	Ser	Gln	Leu	
	105					110		
AGC	CAG	TGT	GAA	TGC	AGA	CCT	AAA	383
Ser	Gln	Cys	Glu	Cys	Arg	Pro	Lys	
120					125			

Fig. 2(ii)

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384	AAA	AAG	GAC	AGT	GCT	GTG	AAG	CCA
	Lys	Lys	Asp	Ser	Ala	Val	Lys	Pro
			130					135
432	CGT	CCC	CAG	CCC	CGT	TCT	GTT	CCG
	Arg	Pro	Gln	Pro	Arg	Ser	Val	Pro
		145					150	
480	CCC	TCC	CCA	GCT	GAC	ATC	ACC	CAT
	Pro	Ser	Pro	Ala	Asp	Ile	Thr	His
	160					165		
528	GCC	CAC	GCT	GCA	CCC	AGC	ACC	ACC
	Ala	His	Ala	Ala	Pro	Ser	Thr	Thr
					180			
576	GCT	GCC	GCT	GCC	GAC	GCC	GCA	GCT
	Ala	Ala	Ala	Ala	Asp	Ala	Ala	Ala
					195			

Fig. 2(iii)

00000-15561E60

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GAC	AGG	GCT	GCC	ACT	CCC	CAC	CAC	431
Asp	Arg	Ala	Ala	Thr	Pro	His	His	
				140				
GGC	TGG	GAC	TCT	GCC	CCC	GGA	GCA	479
Gly	Trp	Asp	Ser	Ala	Pro	Gly	Ala	
			155					
CCC	ACT	CCA	GCC	CCA	GGC	CCC	TCT	527
Pro	Thr	Pro	Ala	Pro	Gly	Pro	Ser	
		170					175	
AGC	GCC	CTG	ACC	CCC	GGA	CCT	GCC	575
Ser	Ala	Leu	Thr	Pro	Gly	Pro	Ala	
	185					190		
TCC	TCC	GTT	GCC	AAG	GGC	GGG	GCT	T 624
Ser	Ser	Val	Ala	Lys	Gly	Gly	Ala	
200					205			

Fig. 2(iv)

11/52

625 AGAGCTCAAC CCAGACACCT GCAGGTGCCG
685 GACTCAGCAG GGTGACTTGC CTCAGAGGCT
745 GGTAATAAAC AGCCAAGCCC CCAAGACCTC
805 GCCTCTCAGA GGGCTCTTCT GCCATCCCTT
865 GAGTTGGAAG AGGAGACTGG GAGGCAGCAA
825 GGAGTACTGT CTCAGTTTCT AACCACTCTG
985 CTCCCCTCAC TAAGAAGACC CAAACCTCTG
1045 CTGTGACCCC CAACCCTGAT AAAAGAGATG

Fig.2(v)

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GAAGCTGCGA AGGTGACACA TGGCTTTTCA	684
ATATCCCAGT GGGGGAACAA AGGGGAGCCT	744
AGCCCAGGCA GAAGCTGCTC TAGGACCTGG	804
GTCTCCCTGA GGCCATCATC AAACAGGACA	864
GAGGGGTCAC ATACCAGCTC AGGGGAGAAT	924
TGCAAGTAAG CATCTTACAA CTGGCTCTTC	984
CATAATGGGA TTTGGGCTTT GGTACAAGAA	1044
GAAGGAAAAA AAAAAAAAAA	1094

Fig.2(vi)

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<i>Fig. 3(i)</i>	<i>Fig. 3(ii)</i>

[illegible]

SCORE = 181 (92.4 BITS), EXPECT = 6.4e-20,
IDENTITIES = 33/75 (44%), POSITIVES = 48/75

```

QUERY:      91  PTGQHQVRMQILMIR  105
              PT  +    + MQI+  I+
SBJCT:      96  PTEESNITMQIMRIK  110

```

```

QUERY:      110  QLGEMSLEEHSQCECRPKK  128
              ++GEMS  +H+  CECRPKK
SBJCT:      116  HIGEMSFLQHNKCECRPKK  134

```

```

QUERY:      202  RCQGRGLELNPDTCRCKRLRR  222
              RC +R LELN  TCRC  K  RR
SBJCT:      195  RCKARQLELNERTCRCDKPRR  215

```

```

QUERY:      187  DPRTCRCRCR  196
              DP+TC+C  C+
SBJCT:      181  DPQTCCKCSCK  190

```

Fig. 3 (i)

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GROWTH FACTOR PRECURSOR (VEGF)

$$P = 6.4e-20$$

(64%)

MGTVAKQLVPSCVTVQRCGGCCPDDGLECV 90
 + PSCV + RCGGCC D+GLECV
 PDEIEYIFKPSCVPLMRCGGCCNDEGLECV 95

$$\text{POISSON } P(2) = 9.1e-12$$

(84%)

$$\text{POISSON } P(3) = 3.6e-18$$

(71%)

$$\text{POISSON } P(4) = 7.3e-10$$

(90%)

Fig. 3(i)

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668020-15601E60

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<p>17/52</p> <p><i>Fig.4(i)</i></p>	<p>18/52</p> <p><i>Fig.4(ii)</i></p>
<p>19/52</p> <p><i>Fig.4(iii)</i></p>	<p>20/52</p> <p><i>Fig.4(iv)</i></p>

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Gap Weight:3.00	Average Match:1.000
Length Weight:0.100	Average Mismatch:-0.900
Quality:100.9	Length:739
Ratio:0.175	Gaps:30
Percent	Percent
Similarity:69.703	Identity:69.703

28	ATGAGCCCTCTGCTCCGCCGCCTGC
17	ATGAACTTTCTGCT.....GTCT..
68	TGCAGCTGGCCCCCGCCCAGGCCCC
57	TGCTGCTCTACCTCCACCATGCCAA
118	CACCAGAGGA.....
106	AGAAGGAGGAGGGCAGAATCATCAC
140	GTGTATACTCGC.GCTACCTGCCAG
152	GTCTATCAGCGCAGCTA.CTGCCAT
194	T....GA.....CTGTGGAGCTCAT
201	TCCAGGAGTACCCTGATGAGATCGA
235	CCCAGCTGCGTGACTGTGCAGCGCT
239	CCATCCTGTGTGCCCCCTGATGCGAT
285	CCTGGAGTGTGTGCCCCACTGGGCAG
289	CCTGGAGTGTGTGCCCCACTGAGGAG

Fig.4(i)

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330CCTCATGATCCGGTACC
339	GGATCAAACCTCA.....C
369	GTCCCTGGAAGAACACAGCCAGTGT
376	GAGCTTCCTACAGCACAAATGT
419	GTGCTGTGAAGCCAGACAGGGCTGC
423	G.....AGCAAGACAAG.....
469	CGTTCTGTTCCGGGCTGGGACTCTG
443	...TGTGGGCCTTGCTCAGA.....
519	CATCACCCATCCCCTCCAGCCCCA
468
569	GC.....ACCACCAGCGCCC
469	GCATTTGTTTGTACAA.....
609	TGCCGACGCCGCAGCTTCCTCCGTT
509	TG.CAAAAACACAGACTC..GCGTT
657	AACCCAGACACCTGCAGGTGCCGGA
554	AACGAACGTACTTGCAGATGTGACA

Fig.4(iii)

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
1	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
2	2	1	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
3	3	2	1	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
4	4	3	2	1	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
5	5	4	3	2	1	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80																				

CGAGCAGTCAGC . . . TGGGGGAGAT	368
CAAG . . GCCAGCACATAGGAGAGAT	375
GAATGCAGACCTAAAAAAAAAAGGACA	418
GAATGCAGACC . . . AAAGAAAGATA	422
CACTCCCCACCACCGTCCCCAGCCC	468
. AAAATCCC	442
CCCCCGGAGCACCTCCCCAGCTGA	518
. . . GCGGAGAA	467
GGCCCCTCTGCCCACGCTGCACCCA	568
. A	468
TGACCCCCGGACCTGCCGCTGCCGC	608
. GATCCGCAGACGTGTAAATGTTCC	508
GCCAAGGGCGGGGC . . TTAGAGCTC	656
GC . . AAGGCGAGGCAGCTTGAGTTA	553
AGCTGCGAAGGTGA	695
AGCCGAGGCGGTGA	592

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<i>22/52</i> <i>Fig.5(i)</i>	<i>23/52</i> <i>Fig.5(ii)</i>	<i>24/52</i> <i>Fig.5(iii)</i>
<i>25/52</i> <i>Fig.5(iv)</i>	<i>26/52</i> <i>Fig.5(v)</i>	<i>27/52</i> <i>Fig.5(vi)</i>

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165SOMSQ.MSF.msf MSF:687
Type: D Tuesday, June 20, 1995
Check:3140

1
VEGF165 ATGAACTTTCTGCTGTCTTGGGTG
SOM175 ATGAGCCCTCTGCTCCGCCGCCTG
SOM175-e6 ATGAGCCCTCTGCTCCGCCGCCTG
SOM175-e6&7 ATGAGCCCTCTGCTCCGCCGCCTG
SOM175-e4 ATGAGCCCTCTGCTCCGCCGCCTG

81
VEGF165 CACCCATGGCAGAAGGAGGAGGGC
SOM175 TGCCCCTGGCCACCAGAGGAAAGT
SOM175-e6 TGCCCCTGGCCACCAGAGGAAAGT
SOM175-e6&7 TGCCCCTGGCCACCAGAGGAAAGT
SOM175-e4 TGCCCCTGGCCACCAGAGGAAAGT

161
VEGF165 CCAATCGAGACCCTGGTGGACATC
SOM175 GTGGTGGTGCCCTTGACTG.TGGA
SOM175-e6 GTGGTGGTGCCCTTGACTG.TGGA
SOM175-e6&7 GTGGTGGTGCCCTTGACTG.TGGA
SOM175-e4 GTGGTGGTGCCCTTGACTG.TGGA

241
VEGF165 GATGCGATGCGGGGGGCTGCTGCAA
SOM175 GCAGCGCTGTGGTGGCTGCTGCCC
SOM175-e6 GCAGCGCTGTGGTGGCTGCTGCCC
SOM175-e6&7 GCAGCGCTGTGGTGGCTGCTGCCC
SOM175-e4 GCAGCGCTGTGGTGGCTGCTGCCC

Fig.5(i)

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CATTGGAGCCTTGCCTTGCTGCTCTACC
CTGCTCGCCGCACTCCTGCAGCTGGCCC
CTGCTCGCCGCACTCCTGCAGCTGGCCC
CTGCTCGCCGCACTCCTGCAGCTGGCCC
CTGCTCGCCGCACTCCTGCAGCTGGCCC

AGAATCATCACGAAGTGGTGAAGTTCAT
GGTGTCATGGATAGATGTGTATACTCGC
GGTGTCATGGATAGATGTGTATACTCGC
GGTGTCATGGATAGATGTGTATACTCGC
GGTGTCATGGATAGATGTGTATACTCGC

TTCCAGGAGTACCCTGATGAGATCGAGT
GCTCATGGGCAACCGTGGCCAAAC . . AGC
GCTCATGGGCAACCGTGGCCAAAC . . AGC
GCTCATGGGCAACCGTGGCCAAAC . . AGC
GCTCATGGGCAACCGTGGCCAAAC . . AGC

TGACGAGGGCCTGGAGTGTGTGCCCCACT
TGACGATGGCCTGGAGTGTGTGCCCCACT
TGACGATGGCCTGGAGTGTGTGCCCCACT
TGACGATGGCCTGGAGTGTGTGCCCCACT
TGACGATGGCCTGGAGTGTGTGCCCCACT

Fig. 5(ii)

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000020 15001E60

80
TCCACCATGCCAAGTGGTCCCAGGCTG.
CCGCCCAGGCCCCTGTCTCCCAGCCTGA
CCGCCCAGGCCCCTGTCTCCCAGCCTGA
CCGCCCAGGCCCCTGTCTCCCAGCCTGA
CCGCCCAGGCCCCTGTCTCCCAGCCTGA

160
GGATGTCTATCAGCGCAGCTACTGCCAT
G.....CTACCTGC.CAGCC.CCGGGAG
G.....CTACCTGC.CAGCC.CCGGGAG
G.....CTACCTGC.CAGCC.CCGGGAG
G.....CTACCTGC.CAGCC.CCGGGAG

240
ACATCTTCAAGCCATCCTGTGTGCCCCCT
TGGTGCCCCAG.....CTGCGTGACTGT
TGGTGCCCCAG.....CTGCGTGACTGT
TGGTGCCCCAG.....CTGCGTGACTGT
TGGTGCCCCAG.....CTGCGTGACTGT

320
GAGGAGTCCAACATCACCATGCAGATTA
GGGCAGCACCAAGTCCGGATGCAGATCC
GGGCAGCACCAAGTCCGGATGCAGATCC
GGGCAGCACCAAGTCCGGATGCAGATCC
GGGCAGCACCAAGTCCGGATGCAGA...

Fig.5(iii)

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000020 15067600

	321
VEGF165	TGCGGATCAAACCTCACCAAGGCC
SOM175	TCATGATCCGG...TACCCGAGCA
SOM175-e6	TCATGATCCGG...TACCCGAGCA
SOM175-e6&7	TCATGATCCGG...TACCCGAGCA
SOM175-e4
	401
VEGF165	AAGAAAGATAG.....AGCAA
SOM175	AAAAAGGACAGTGCTGTGAAGCCA
SOM175-e6	AAAAAGGACAGTGCTGTGAAGCCA
SOM175-e6&7	AAAAAGGACAGTGCTGTGAAGCCA
SOM175-e4	AAAAAGGACAGTGCTGTGAAGCCA
	481
VEGF165AAGCA.....
SOM175	CTCTGCCCCCGGAGCACCCCTCCCC
SOM175-e6
SOM175-e6&7
SOM175-e4	CTCTGCCCCCGGAGCACCCCTCCCC
	561
VEGF165	A.....GATCCGCA
SOM175	GCACCACCAGCGCCCTGACCCCCG
SOM175-E6	GCACCACCAGCGCCCTGACCCCCG
SOM175-e6&7
SOM175-e4	GCACCACCAGCGCCCTGACCCCCG
	641
VEGF165	TTGAGTTAAACGAACGTACTTGCA
SOM175	TAGAGCTCAACCCAGACACCTGCA
SOM175-e6	TAGAGCTCAACCCAGACACCTGCA
SOM175-e6&7
SOM175-e4	TAGAGCTCAACCCAGACACCTGCA

Fig.5(iv)

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AGCACATAGGAGAGATGAGCTTCCTACA
GTCAGCTGGGGGAGATGTCCCTGGAAGA
GTCAGCTGGGGGAGATGTCCCTGGAAGA
GTCAGCTGGGGGAGATGTCCCTGGAAGA
.....

GACAAGAA....AATCCCTGTGG.....
GACAGGGCTGCCACTCCCCACCACCGTC
GATAG.....
GATAG.....
GACAGGGCTGCCACTCCCCACCACCGTC

.....
AGCTGACATCACCCATCCCCTCCAGCC
.....CC
.....
AGCTGACATCACCCATCCCCTCCAGCC

GACGTGTAAATGTTCTCTGCAAAAAC.AC
GACCTGCCGCTGCCGCTGCCGACGCCGC
GACCTGCCGCTGCCGCTGCCGACGCCGC
.....
GACCTGCCGCTGCCGCTGCCGACGCCGC

687

GATGTGACAAGCCGAGGCGGTGA
GGTGCCGGAAGCTGCGAAGGTGA
GGTGCCGGAAGCTGCGAAGGTGA
.GTGCCGGAAGCTGCGAAGGTGA
GGTGCCGGAAGCTGCGAAGGTGA

Fig.5(v)

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400

GCACAACAAATGTGAATGCAGACC...A
 ACACAGCCAGTGTGAATGCAGACCTAAA
 ACACAGCCAGTGTGAATGCAGACCTAAA
 ACACAGCCAGTGTGAATGCAGACCTAAA
CCTAAA

480

.....GCCTTGCTCAGAGCGGAGA
 CCCAGCCCCGTTCTGTTCCGGGCTGGGA

 CCCAGCCCCGTTCTGTTCCGGGCTGGGA

560

.....TTTGTT.....TGTAC..A
 CCAGGCCCTCTGCCCACGCTGCACCCA
 CCAGGCCCTCTGCCCACGCTGCACCCA

 CCAGGCCCTCTGCCCACGCTGCACCCA

640

AGACTCG..CGTTGCAAGGCGAGGCAGC
 AGCTTCCTCCGTTGCCAAGGGCGGGGCT
 AGCTTCCTCCGTTGCCAAGGGCGGGGCT

 AGCTTCCTCCGTTGCCAAGGGCGGGGCT

Fig.5(vi)

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<p><i>Fig 6(i)</i></p> <p>29/52</p>	<p><i>Fig 6(ii)</i></p> <p>30/52</p>
<p><i>Fig 6(iii)</i></p> <p>31/52</p>	

29/52

VEGF ₁₆₅	M	N	F	L	L	S	W	V	H	W	S	L	A	L	L	Y	L	H	H	A	K	W	S	Q	A	A	P	
SOM175 _{Short}	M	S	P	L	L	R	R	L	.	.	.	L	A	A	L	L	Q	L	A	P	A	Q	A	P
VEGF ₁₆₅	I	F	Q	E	Y	P	D	E	I	E	Y	I	F	K	P	S	C	V	P	L	M	R	C	G	G	C	C	N
SOM175 _{Short}	L	T	V	E	L	M	G	T	V	A	K	Q	L	V	P	S	C	V	T	V	Q	R	C	G	G	C	C	P
VEGF ₁₆₅	F	L	Q	H	N	K	C	E	C	R	P	K	K	D	R	A
SOM175 _{Short}	L	E	E	H	S	Q	C	E	C	R	P	K	K	K	D	S	A	V	K	P	D	R	A	A	T	P	H	H
VEGF ₁₆₅	C	K	C	S	C	K	N	T	D	S	R	C	K	A	R	Q	L	E	L	N	E	R	T	C	R	C	D	K
SOM175 _{Short}	H	A	A	P	S	T	S	A	L	T	P	G	P	A	A	A	A	A	A	D	A	A	A	S	S	V	A	K

OR...

VEGF ₁₆₅	M	N	F	L	L	S	W	V	H	W	S	L	A	L	L	L	Y	L	H	H	A	K	W	S	Q	A	A	P
SOM175 _{Long}	M	S	P	L	L	R	R	L	.	.	.	L	A	A	L	L	Q	L	A	P	A	Q	A	P
VEGF ₁₆₅	I	F	Q	E	Y	P	D	E	I	E	Y	I	F	K	P	S	C	V	P	L	M	R	C	G	G	C	C	N
SOM175 _{Long}	L	T	V	E	L	M	G	T	V	A	K	Q	L	V	P	S	C	V	T	V	Q	R	C	G	G	C	C	P
VEGF ₁₆₅	F	L	Q	H	N	K	C	E	C	R	P	K	K	D	R	A
SOM175 _{Long}	L	E	E	H	S	Q	C	E	C	R	P	K	K	K	D	S	A	V	K	P	D	R	A	A	T	P	H	H
VEGF ₁₆₅	G	P	C	S	E	R	R	K	H	L	F	V	Q	D	P	Q	T	C	K	C	S	C	K	N	T	D	S	.
SOM175 _{Long}	P	R	C	T	Q	H	H	Q	R	.	.	.	P	D	P	R	T	C	R	C	R	C	R	R	R	S	F	L

Fig.6(i)

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M A E G G Q N H H E . V V K F M D V Y Q R S Y C H P I E T L V D 60
 V S Q P D A P G H Q R K V V S W I D V Y T R A T C C P R E V V P 55
 D E G L E C V P T E E S N I T M Q I M R I K P H Q G Q H I G E M S 121
 D G L E C V P T G Q H Q V T R M Q I L M I R . Y P S S Q L G E M S 115
 R Q E N P C G P C S E R R K H L F . V Q D P Q T 170
 R P Q P R S V P G W D S A P G A P S P A D I T H P T P A P G P S A 175
 P R R
 G G A

191
207

M A E G G Q N H H E . V V K F M D V Y Q R S Y C H P I E T L V D 60
 V S Q P D A P G H Q R K V V S W I D V Y T R A T C C P R E V V P 55
 D E G L E C V P T E E S N I T M Q I M R I K P H Q G Q H I G E M S 121
 D G L E C V P T G Q H Q V T R M Q I L M I R . Y P S S Q L G E M S 115
 R Q E N P S A P G A P S P A D I T H P T P A P G P L C 170
 R P Q P R S V P G W D S A P G A P S P A D I T H P T P A P G P L C 177
 R C K A R Q L E L N E R T C R C D K P R R 191
 R C Q G R G L E L N P D T C R C R K L R R 222

Fig. 6(ii)

Homology of SOM175 to VEGF₁₆₅ is 27% (33%) at the protein level, however within this are blocks of 100% homology. In particular, many structural residues are conserved including those thought to be involved in homodimerisation of VEGF (by comparison with PDGF).
ie. Cysteine-47

Cysteine-47

Proline-70, Cysteine-72, Valine-74

Arginine-77, Cystein-78, Glycine-80, Valine-74,

Cysteine-89, Proline-91

Cysteines 122 & 124

Cysteines-81 & 82

Fig. 6(iii)

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SPLICE VARIANTS OF SOM175

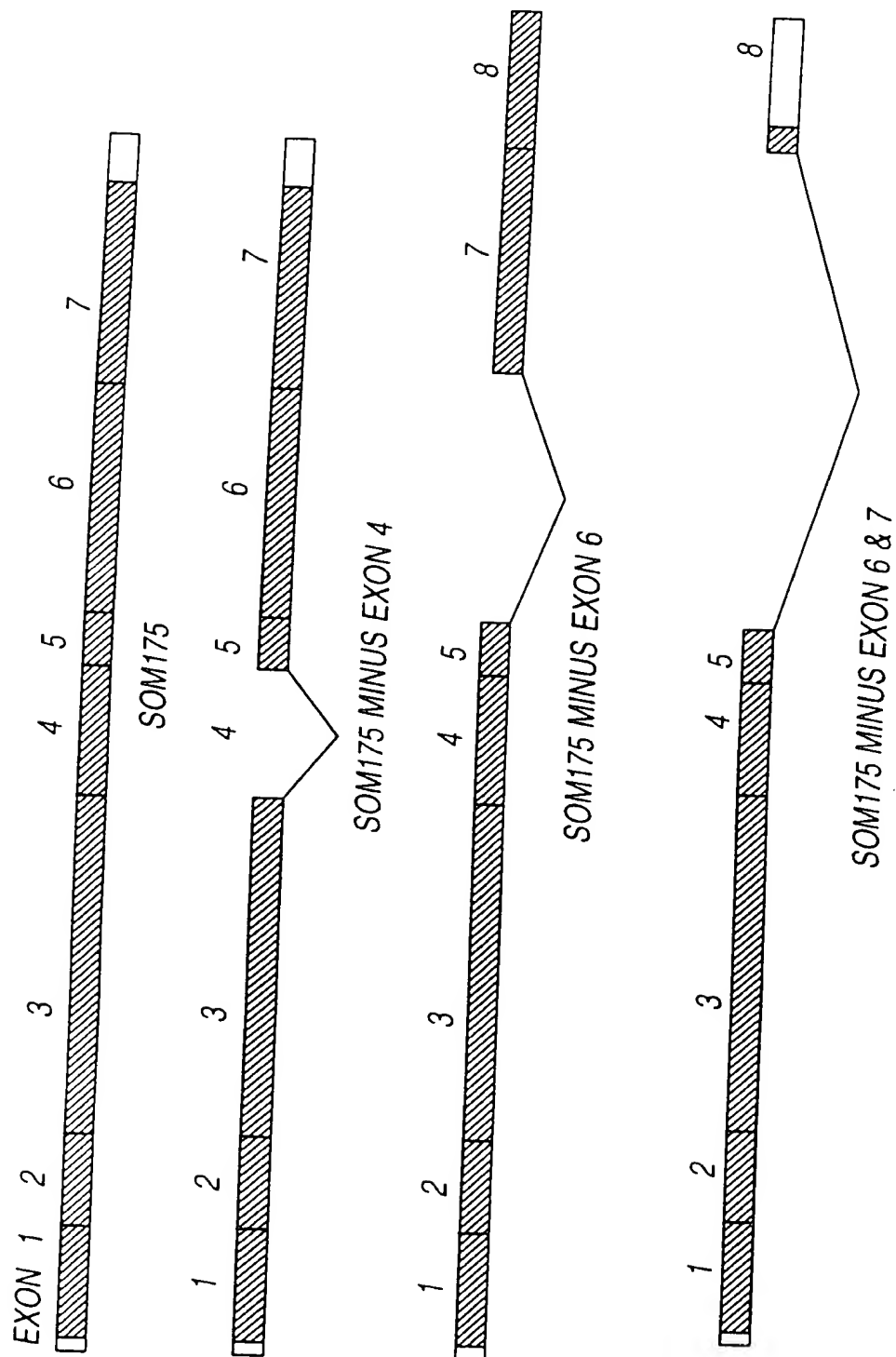


Fig. 7

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GENOMIC STRUCTURE OF HUMAN SOM175

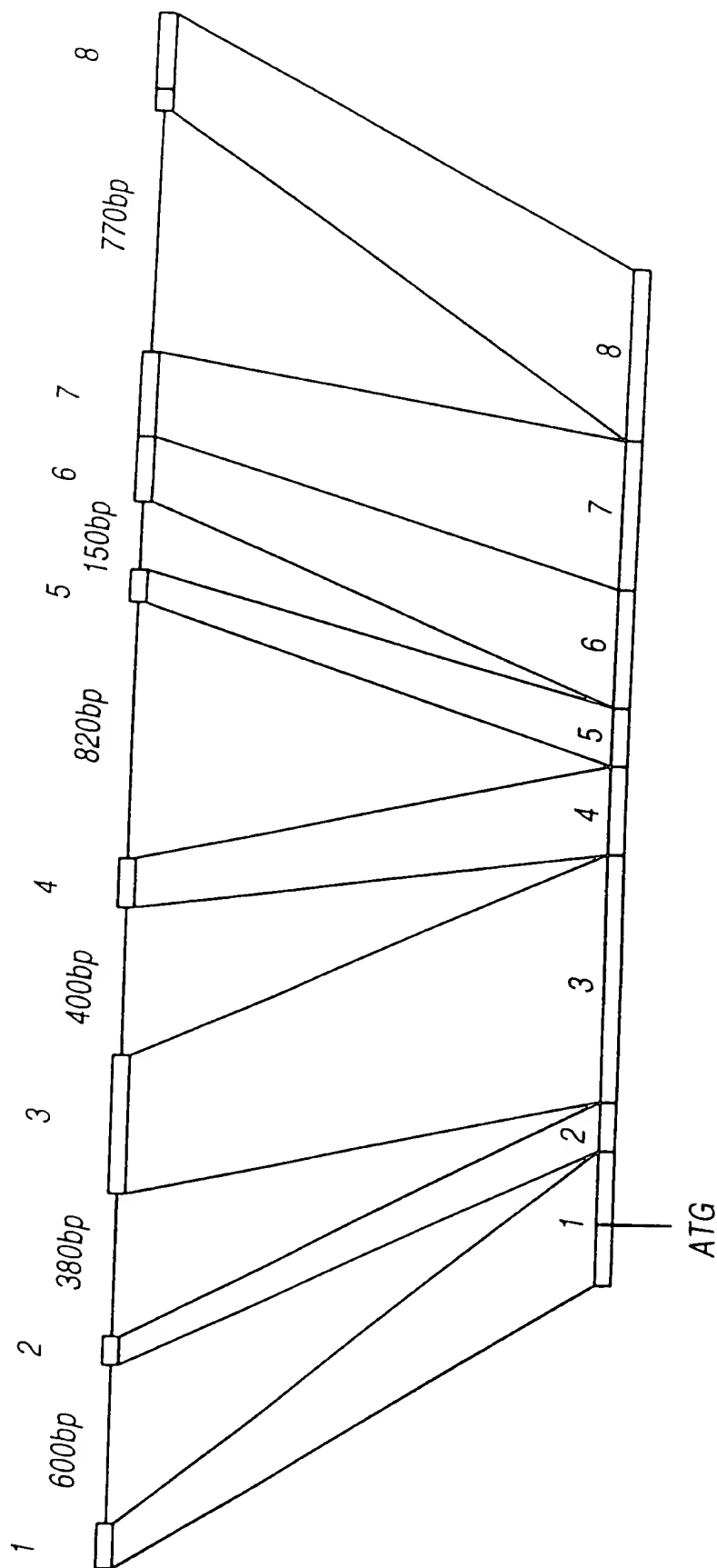


Fig. 8A

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5' UTR...	ATGAGG	*Exon 1 (60bp)	GGCCAG	gtacgtgagg
tctcccacag	GCCCCT	Exon 2 (43bp)	GGAAAG	aatacttaca
tctgctccca	TGGTGT	Exon 3 (187bp)	ATGCAG	gtccgagatg
ctgaatacag	ATCCTC	Exon 4 (73bp)	ATGCAG	gtgtcaggca
acttttcaag	ACCTAA	Exon 5 (34bp)	AGACAG	gtgagtccttt
ctcctccgta	GGCTGC	Exon 6 (101bp)	CTCCAG	ccccaggccc
cccactccag	CCCCAG	Exon 7 (109bp)	ACCCAG	acacctgtag
ccctgctcag	GTGCCG	*Exon 8 (22bp)	AGGTGA	...3'UTR

Fig.8B

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<p>36/52</p> <p><i>Fig. 9(i)</i></p>	<p>37/52</p> <p><i>Fig. 9(ii)</i></p>
<p>38/52</p> <p><i>Fig. 9(iii)</i></p>	<p>39/52</p> <p><i>Fig. 9(iv)</i></p>

653020-15651160

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-163 gcacgagctcaggccgctcgctgcggcgctg
-103 gggggccgcggaggagccgccccctgcgcc
-43 ggcggctctggctgacccccccccacaccg

16 CGTCGCCTGCTGCTTGTTGCACTGCTGCAG
R R L L L V A L L Q

76 TTTGATGGCCCCAGTCACCAGAAGAAAGTG
F D G P S H Q K K V

136 ACATGCCAGCCCAGGGAGGTGGTGGTGCCT
T C Q P R E V V V P

196 AAACAAGTAGTGCCCAGCTGTGTGACTGTG
K Q L V P S C V T V

256 GGCCTGGAATGTGTGCCCACTGGGCAACAC
G L E C V P T G Q H

316 TACCCGAGCAGTCAGCTGGGGGAGATGTCC
Y P S S Q L G E M S

376 CCTAAAAAAAAAGGAGAGTGCTGTGAGGCCA
P K K K E S A V R P

436 CAGCCCCGCTCTGTTCCGGGCTGGGACTCT
Q P R S V P G W D S

Fig.9(i)

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cgttgcgctgcctgcgcccaggggctcgggga	
ccgccccgggtccccgggtccgcgcgccatgg	
ccgggctagggccccgATGAGCCCCCTGCTG	
	M S P L L -17
CTGGCTCGCACCCAGGCCCTGTGTCCCAG	
L A R T Q A P V S Q	4
GTGCCATGGATAGACGTTTATGCACGTGCC	
V P W I D V Y A R A	24
CTGAGCATGGAACATGGGCAATGTGGTC	
L S M E L M G N V V	44
CAGCGCTGTGGTGGCTGCTGCCCTGACGAT	
Q R C G G C C P D D	64
CAAGTCCGAATGCAGATCCTCATGATCCAG	
Q V R M Q I L M I Q	84
CTGGGAGAACACAGCCAATGTGAATGCAGA	
L G E H S Q C E C R	104
GACAGGGTTGCCATACCCCACCGTCCC	
D R V A I P H H R P	124
ACCCCGGGAGCACCTCCCCAGCTGACATC	
T P G A P S P A D I	144

Fig.9(ii)

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496	ATCCATCCC <u>ACTCCAG</u> CCCCAGGATCCTCT
	I H P T P A P G S S
	S P R I L
556	CTGACCCCCGGACCTGCCGTTGCCGCTGTA
	L T P G P A V A A V
	P D P R T C R C R C
616	GGGGCTTAGAGCTCAACCCAGACACCTGTA
	G A *
	R G L E L N P D T C
676	ctttccagactccacgggccccgggctgcttt
736	agcacaggcgtaacctcctcagtctgggag
796	gagctctctcgccatcttttatctcccaga
856	atgtctcacctcaggggcccagggtactctc
916	ttctgggctgggctgtctcccctcactatgaa
976	gggttctgttatgataactgtgacacacac
1036	gacactaaaaaaaaaaaaaaaaaaaaaaaaaa

Fig.9(iii)

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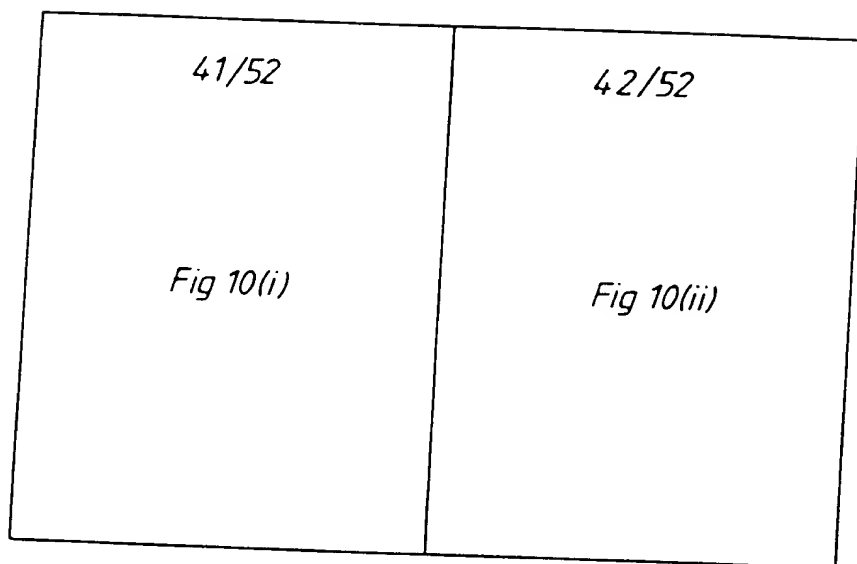
GCCCGCCTTGCACCCAGCGCCGCCAACGCC
 A R L A P S A A N A 164
 C P P C T Q R R Q R 130

GACGCCGCCGCTTCCTCCATTGCCAAGGGC
 D A A A S S I A K G 184
 R R R R F L H C Q G 150

↓
 GGTGCCGGAAGCCGCGAAAGTGAcaagctg
 R C R K P R K * 186
 167

tatggccctgcttcacagggagaagagtgg
 gtcactgccccaggacctggacctttttaga
 gctgccatctaacaattgtcaaggaacctc
 tcaacttaaccaccctgggtcaagtgagcatc
 aaccccaaacttctaccaataacgggattt
 acacactcacactctgataaaaagagatgga
 aaaaaaaaaaaaaa

Fig.9(iv)



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A

hVRF167	-21	MSPLLRRLLLAALLQLAPAQAP	↓
mVRF167	-21	MSPLLRRLLLVALLQLARTQAP	
hVRF167	30	EVVVPLTVELMGTVAKQLVPSC	
		:	
mVRF167	30	EVVVPLSMELMGNVVKQLVPSC	
hVRF167	80	ILMIRYPSSQLGEMSLEEHSQC	
		:	
mVRF167	80	ILMIQYPSSQLGEMSLGEHSQC	
hVRF167	130	RPDPRTCRCRCRRRSFLRCQGR	
		:	
mVRF167	130	RPDPRTCRCRCRRRRFLHCQGR	

B

hVRF186	116	RAATPHHRPQPRSVPGWDSAPG	
mVRF186	116	RVAIPHHRPQPRSVPGWDSTPG	
hVRF186	166	TPGPAAAAADAAASSVAKGGA*	
		:	
mVRF186	166	TPGPAAVAVDAAASSIAKGGA*	

Fig.10(i)

665020-1551200

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VSQPDAPGHQRKVVSVIDVYTRATCQPR 29

||| | : | : | : | | | | | | | | | |

VSQFDGPSHQKKVVPWIDVYARATCQPR 29

VTVQRCGGCCPDDGLECVPTGQHQVRMQ 79

||| | | | | | | | | | | | | | | | | | | |

VTVQRCGGCCPDDGLECVPTGQHQVRMQ 79

ECRPKKKDSAVKPDSPRPLCPRCTQHHQ 129

||| | | | | : | | | : | | | | | | | | | : : |

ECRPKKKESAVRPDSPRILCPPCTQRRQ 129

GLELNPDTCRCKLRR* 167

||| | | | | | | | | | | | | :

GLELNPDTCRCKPRK* 167

APSPADITHPTPAPGPSAHAAPSTTSAL 165

||| | | | | | | | | | | | : | | | | |

APSPADIIHPTPAPGSSARLAPSAANAL 165

186

186

Fig.10(ii)

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Fig 11(i)	Fig 11(ii)

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mVRF167	-21	MSPLLRRLL..LLVALLQL..
		: : :
mVEGF188	-26	MNFLLSWVHWTLALLLYLHH
mVRF167	25	TCQPREVVVPLSMELMGNVV
		: : : : :
mVEGF188	24	YCRPIETLVDIFQEYPDEIE
mVRF167	75	QVRMQILMIQYPSSQ.LGEM
		: : :
mVEGF188	74	NITMQIMRIKPHQSQHIGEM
mVRF167	119ILCPPC
		:
mVEGF188	124	QKRKRKKSFRKSWSVHCEPC
mVRF167	152	GLELNPDTCRCKPRK
		: :
mVEGF188	173	QLELNERTCRCDKPRR

Fig.11(i)

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AR.TQAPVSQFDGPSHQKKVVPWIDVYARA	24
: : : : : : ::	
AKWSQAAPTT.EGEQKSHEVIKFMDVYQRS	23
KQLVPSCVTVQRCGGCCPDDGLECVPTGQH	74
: : : : : : :	
YIFKPSCVPLMRCAGCCNDEALECVPTSES	73
SLGEHSQCECRPKKKESAVRPDSPR.....	118
: :	
SFLQHSRCECRPKKDRTKPEKKSVRGKGKG	123
TQRRQR...PDPRTCRCRCRRRRFLHCQGR	151
: : : : : :	
SERRKHLFVQDPQTCKCSCKNTDS.RCKAR	172
	167
	188

Fig. 11 (ii)

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653340 15664660

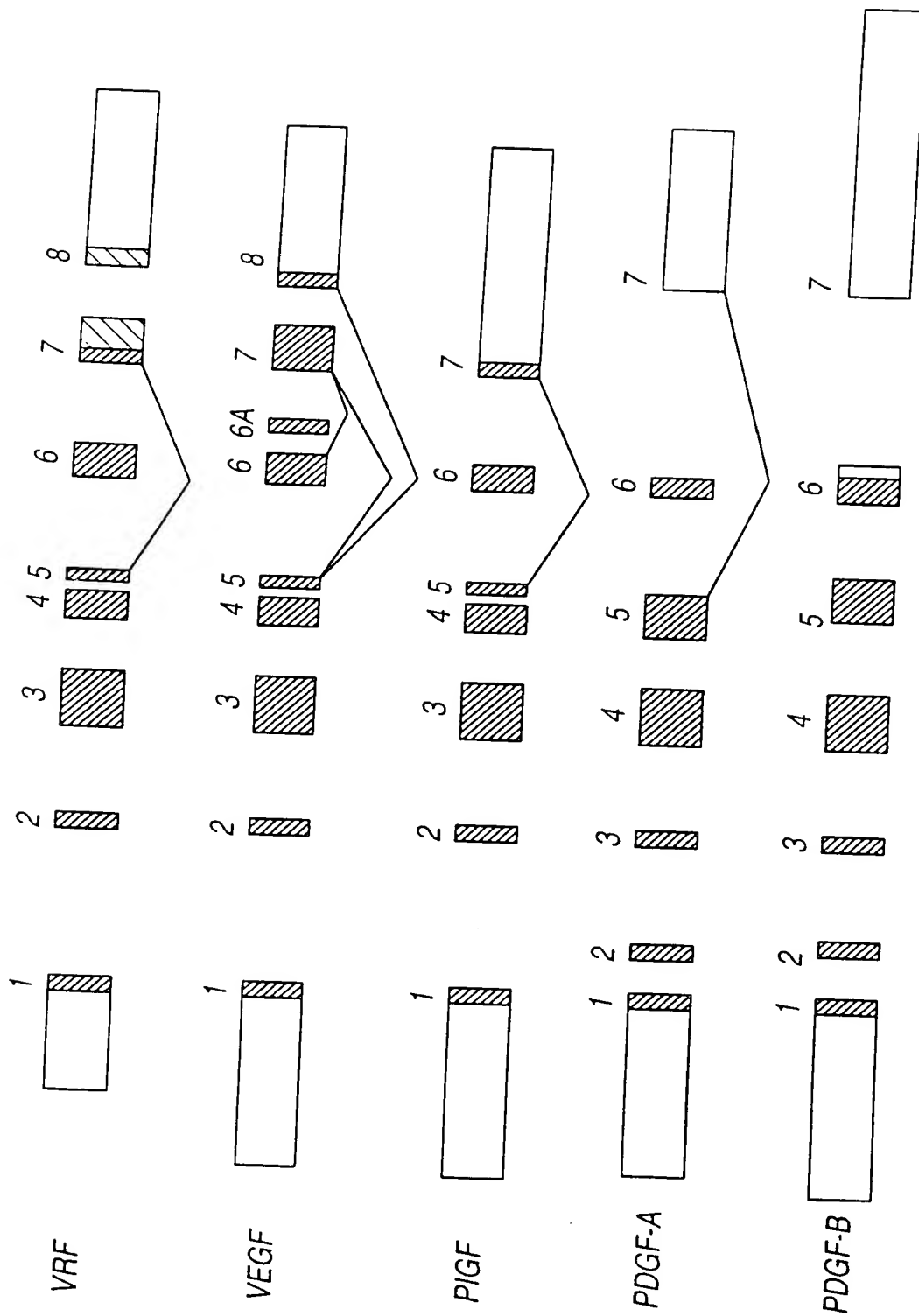


Fig.12

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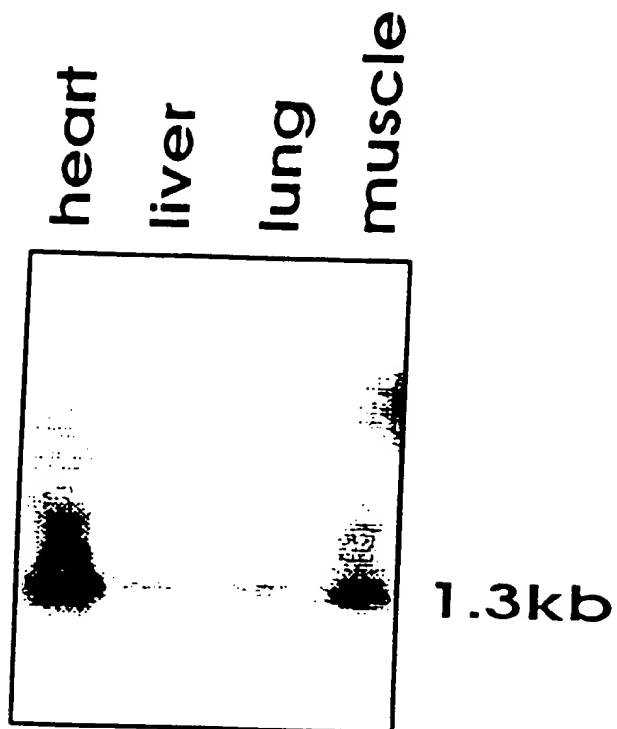


Fig.13

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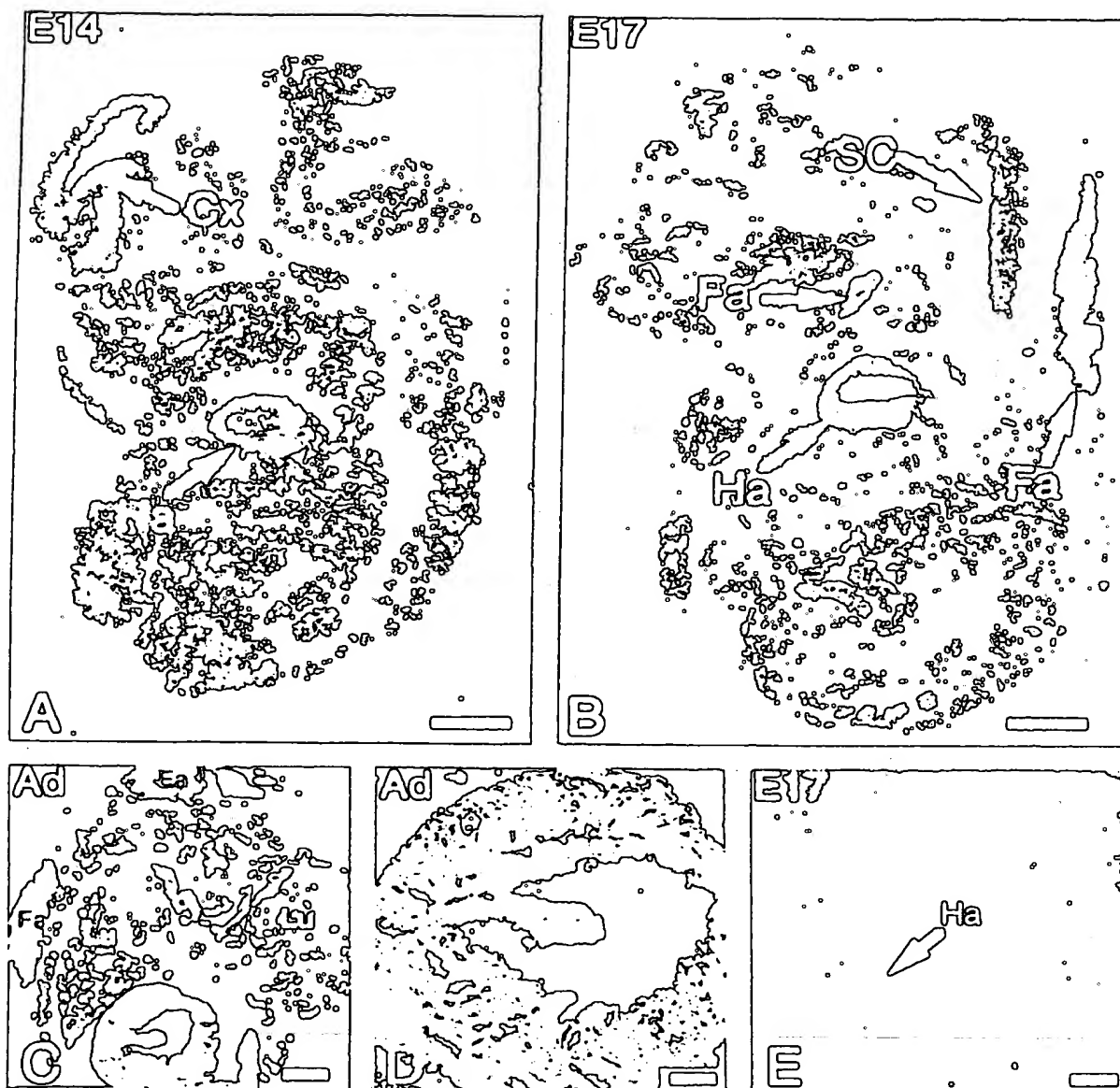


Fig.14

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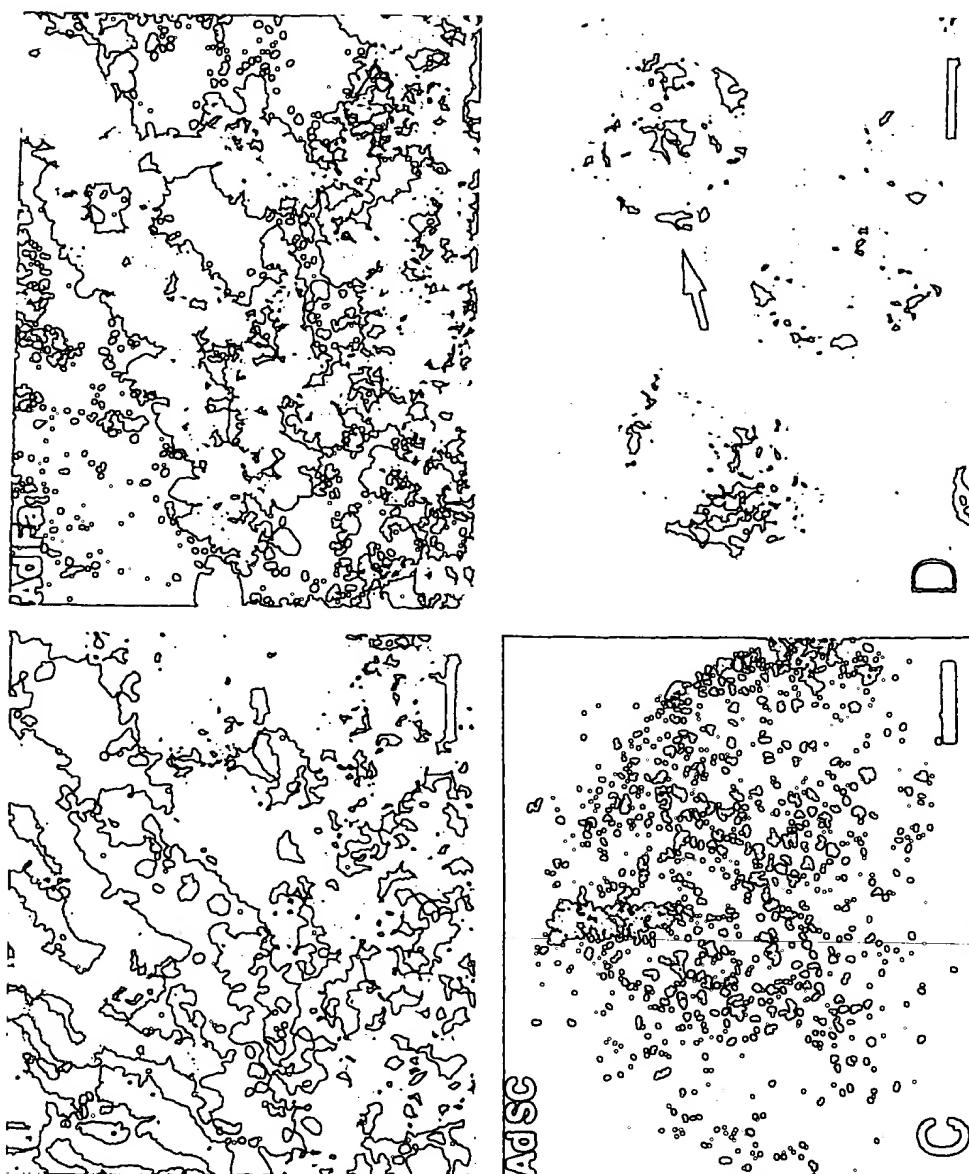


Fig. 15

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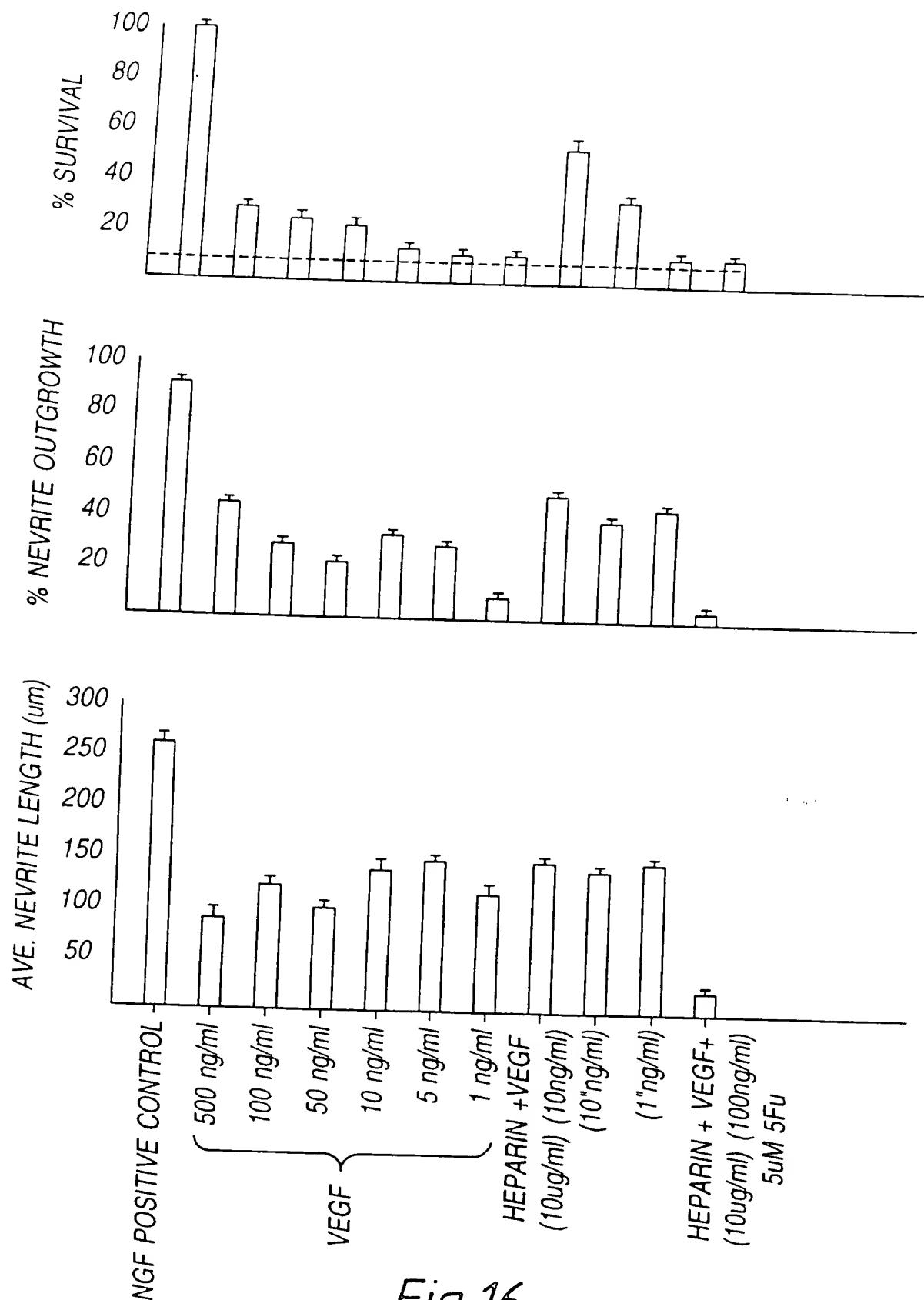


Fig. 16

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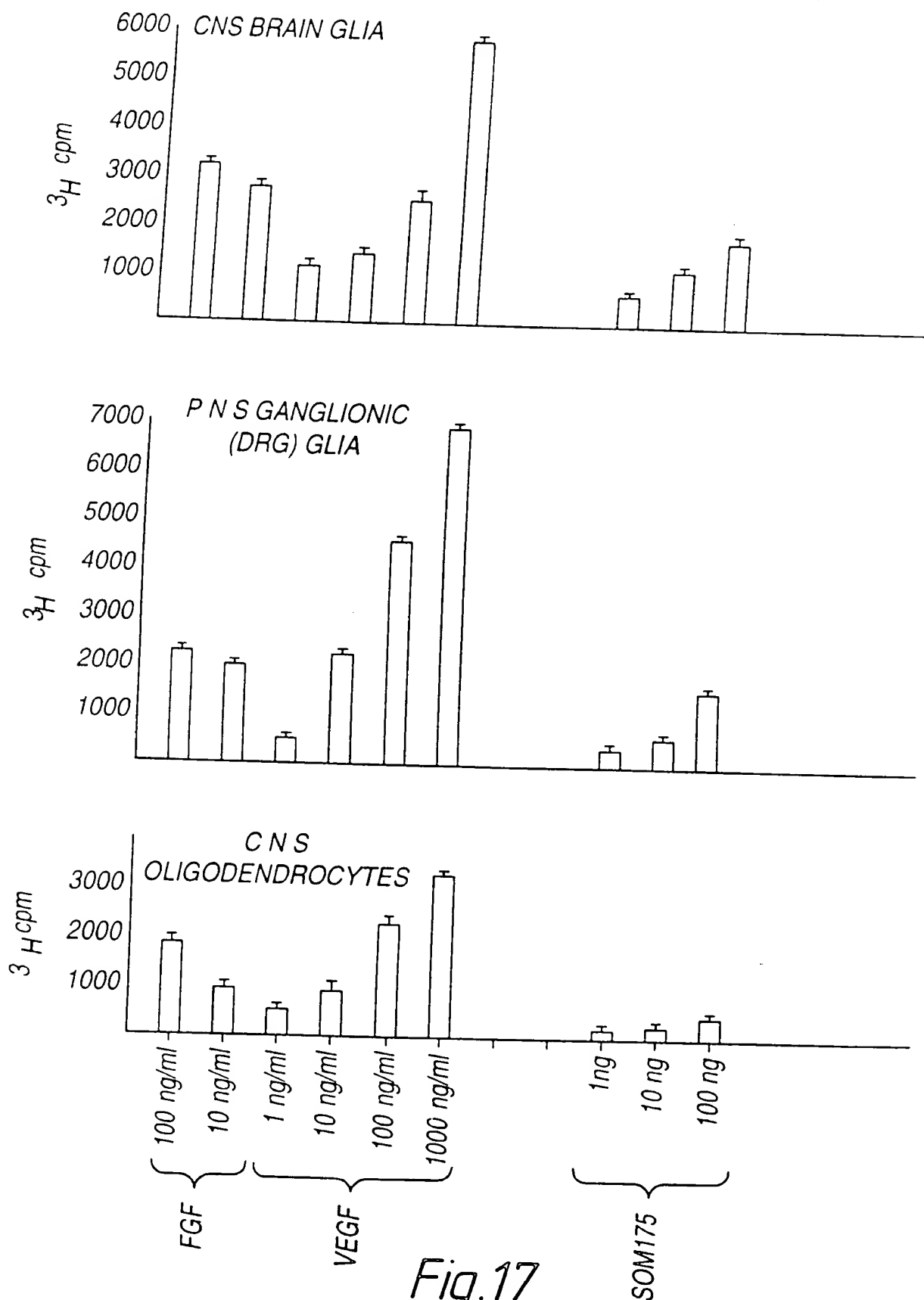


Fig.17

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MOUSE ASTROGLIAL CELLS

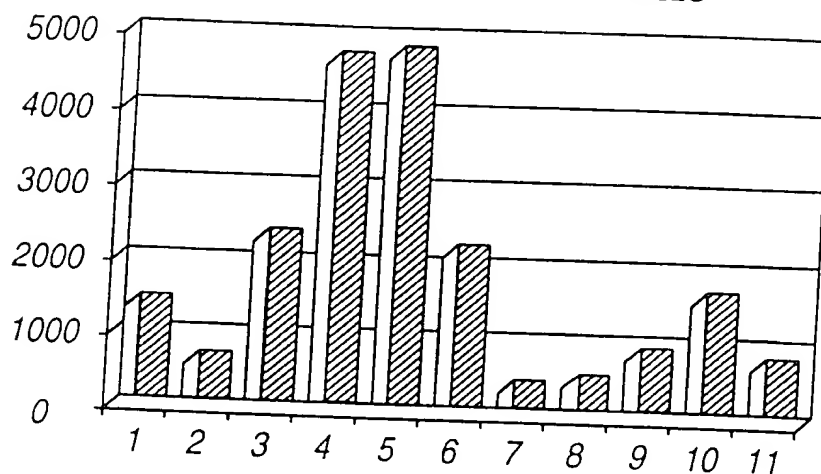


Fig.18

MOUSE OLIGODENDROGLIAL CELLS

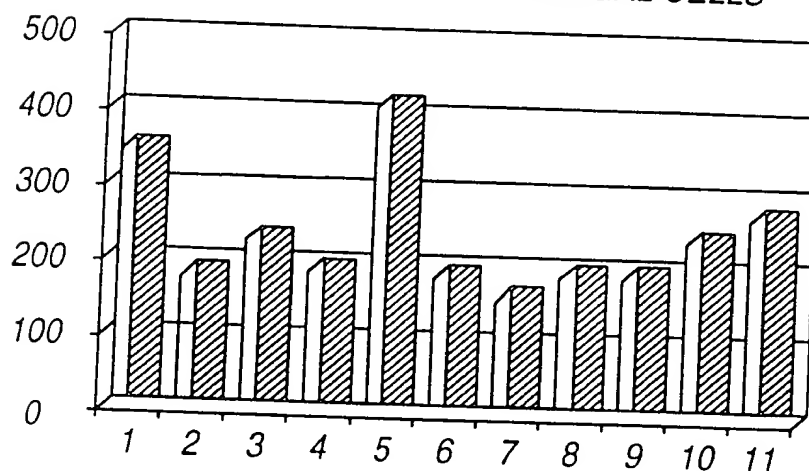


Fig.19

MOUSE FOREBRAIN NEURONS

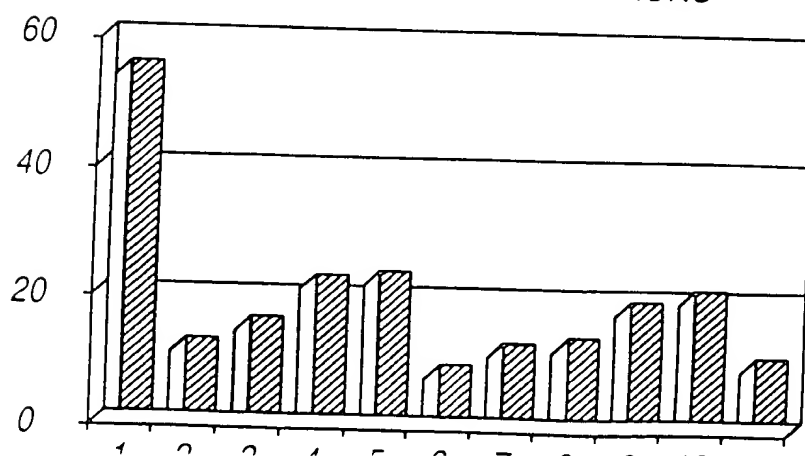


Fig.20